



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WOZNEY, John
CELESTE, Anthony J.
THIES, R. Scott
YAMAJI, Noboru
- (ii) TITLE OF INVENTION: RECEPTOR PROTEINS
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute Inc.- Legal Affairs
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/123,934
 - (B) FILING DATE: 17-SEP-1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: LAZAR, Steven R
 - (B) REGISTRATION NUMBER: 32,618
 - (C) REFERENCE/DOCKET NUMBER: 5203
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617 876 1170
 - (B) TELEFAX: 617 876 5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: CFK1-23a
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 61..1656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGTGGATC CCCCAGGCTG CAGGAATTCT GCGGCCGCCA GGACACGTGC GAATTGGACA	60
ATG ACT CAG CTA TAC ACT TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe 1 5 10 15	108
ATC ATT TCT CAT GTT CAA GGG CAG AAT CTA GAT AGT ATG CTC CAT GGT Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly 20 25 30	156
ACT GGT ATG AAA TCA GAC GTG GAC CAG AAG AAG CCG GAA AAT GGA GTG Thr Gly Met Lys Ser Asp Val Asp Gln Lys Lys Pro Glu Asn Gly Val 35 40 45	204
ACG TTA GCA CCA GAG GAC ACC TTA CCT TTC TTA AAA TGC TAT TGC TCA Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser 50 55 60	252
GGA CAC TGC CCA GAT GAC GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly 65 70 75 80	300
CAT TGC TTT GCC ATT ATA GAA GAA GAT GAT CAG GGA GAA ACC ACG TTA His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu 85 90 95	348
ACT TCT GGG TGT ATG AAG TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp 100 105 110	396
TCA CCA AAA GCC CAG CTA CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn 115 120 125	444
TTG TGC AAC CAA TAT TTG CAG CCT ACA CTG CCC CCT GTC GTT ATA GGC Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly 130 135 140	492
CCA TTC TTT GAT GGC AGC GTC CGA TGG CTG GCT GTG CTC ATC TCT ATG Pro Phe Phe Asp Gly Ser Val Arg Trp Leu Ala Val Leu Ile Ser Met 145 150 155 160	540
GCT GTC TGT ATT GTC GCC ATG ATC GTC TTC TCC AGC TGC TTC TGT TAC Ala Val Cys Ile Val Ala Met Ile Val Phe Ser Ser Cys Phe Cys Tyr 165 170 175	588
AAA CAT TAC TGT AAG AGT ATC TCA AGC AGA GGT CGT TAC AAC CGT GAC Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp 180 185 190	636
TTG GAA CAG GAT GAA GCA TTT ATT CCA GTA GGA GAA TCA CTG AAA GAC Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp 195 200 205	684
CTG ATT GAC CAG TCA CAA AGC TCT GGT AGT GGA TCT GGA TTA CCT TTA Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu 210 215 220	732

TTG	GTT	CAG	CGA	ACT	ATT	GCC	AAA	CAG	ATT	CAG	ATG	GTT	CGG	CAG	GTT	780
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	
225					230					235					240	
GGT	AAG	GGC	CGG	TAT	GGA	GAA	GTA	TGG	ATG	GGT	AAA	TGG	CGT	GGT	GAA	828
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	
				245					250					255		
AAA	GTG	GCT	GTC	AAA	GTA	TTT	TTT	ACC	ACT	GAA	GAA	GCT	AGC	TGG	TTT	876
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	
			260					265					270			
AGA	GAA	ACA	GAA	ATC	TAC	CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	924
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	
		275					280					285				
CTT	GGT	TTT	ATA	GCT	GCA	GAC	ATT	AAA	GGC	ACC	GGT	TCC	TGG	ACT	CAG	972
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr		Ser	Trp	Thr	Gln	
	290					295					300					
CTG	TAT	TTG	ATT	ACT	GAT	TAC	CAT	GAG	AAT	GGG	TCT	CTC	TAT	GAC	TTC	1020
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	
305					310					315					320	
CTG	AAA	TGT	GCC	ACC	CTG	GAC	ACC	AGA	GCC	CTA	CTC	AAG	TTA	GCT	TAT	1068
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	
				325					330					335		
TCT	GCT	GCC	TGT	GGT	CTG	TGC	CAC	CTC	CAC	ACA	GAA	ATT	TAT	GGC	ACG	1116
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	
			340					345					350			
CAA	GGC	AAG	CCT	GCA	ATT	GCT	CAT	CGA	GAC	CTG	AAG	AGC	AAA	AAC	ATC	1164
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	
		355					360					365				
CTT	ATT	AAG	AAA	AAT	GGT	AGT	TGC	TGT	ATT	GCT	GAC	CTG	GGC	CTA	GCT	1212
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	
	370					375					380					
GTT	AAA	TTC	AAC	AGT	GAC	ACA	AAT	GAA	GTT	GAC	ATA	CCC	TTG	AAC	ACC	1260
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr	
385					390					395					400	
AGG	GTG	GGC	ACC	AGG	CGG	TAC	ATG	GCT	CCA	GAA	GTG	CTG	GAC	GAG	AGC	1308
Arg	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser	
				405				410						415		
CTG	AGT	AAA	AAC	CAT	TTC	CAG	CCC	TAC	ATC	ATG	GCT	GAC	ATC	TAC	AGC	1356
Leu	Ser	Lys	Asn	His	Phe	Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser	
			420					425					430			
TTT	GGT	TTG	ATC	ATT	TGG	GAG	ATG	GCC	CGT	CGC	TGT	ATT	ACA	GGA	GGA	1404
Phe	Gly	Leu	Ile	Ile	Trp	Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly	
		435					440					445				
ATC	GTG	GAG	GAA	TAT	CAA	TTA	CCA	TAT	TAC	AAC	ATG	GTG	CCT	AGT	GAC	1452
Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp	
	450					455					460					

CCA TCT TAT GAA GAC ATG CGT GAG GTC GTG TGT GTG AAA CGC TTG CGG	1500
Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg	
465 470 475 480	
CCA ATC GTC TCT AAC CGC TGG AAC AGT GAT GAA TGT CTT CGA GCC GTT	1548
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val	
485 490 495	
TTG AAG CTG ATG TCA GAA TGC TGG GCC CAT AAT CCA GCA TCC AGA CTC	1596
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu	
500 505 510	
ACA GCT TTG AGA ATC AAG AAG ACG CTC GCA AAG ATG GTT GAA TCC CAG	1644
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln	
515 520 525	
GAT GTA AAG ATT TGACAAACAG TTTTGAGAAA GAATTTAGAC TGCAAGAAAT	1696
Asp Val Lys Ile	
530	
TCACCCGAGG AAGGGTGGAG TTAGCATGGA CTAGGATGTC GGCTTGGTTT CCAGACTCTC	1756
TCCTCTACCA TCTTCACAGG CTGCTAACAG TAAACCTTTC AGGACTCTGC AGAATGC	1813

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe	
1 5 10 15	
Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly	
20 25 30	
Thr Gly Met Lys Ser Asp Val Asp Gln Lys Lys Pro Glu Asn Gly Val	
35 40 45	
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser	
50 55 60	
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly	
65 70 75 80	
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu	
85 90 95	
Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp	
100 105 110	
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn	
115 120 125	
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly	
130 135 140	

Pro Phe Phe Asp Gly Ser Val Arg Trp Leu Ala Val Leu Ile Ser Met
 145 150 155 160
 Ala Val Cys Ile Val Ala Met Ile Val Phe Ser Ser Cys Phe Cys Tyr
 165 170 175
 Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp
 180 185 190
 Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
 195 200 205
 Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
 210 215 220
 Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
 225 230 235 240
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
 245 250 255
 Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
 260 265 270
 Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
 275 280 285
 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
 290 295 300
 Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
 305 310 315 320
 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
 325 330 335
 Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
 340 345 350
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
 355 360 365
 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
 370 375 380
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr
 385 390 395 400
 Arg Val Gly Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Ser Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480

Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
485 490 495

Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
500 505 510

Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
515 520 525

Asp Val Lys Ile
530

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: CFK1-43a

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 247..1752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGGCCGCGC CGGCGTGGTG CTCGGAGTGC GGGCGCCGAG GACCCGGGAC CAGGGGCGCG	60
GCGGCGGGTT GGAGTTCAAG GTACTCGTTA CGTGTGACGA GGAAGTGAAG CCCATTCCAT	120
GCCTTGCTGA GAAAGGTTCA AACTTCGGCT GAATCACAAC CATTGGCGC TGAGCTATGA	180
CAAGAGAGCA AACAAAAAGT TAAAGGAGCA ACTCGGCCAT AAGTGACAGA GAAGTTCGTT	240
GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG	288
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys	
1 5 10	
AAG GAG GAT GGT GAG AGT ACA GCC CCC ACT GCT CGG CCC AAG GTC CTG	336
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Ala Arg Pro Lys Val Leu	
15 20 25 30	
CGT TGT AAA TGC CAC CAC CAC TGT CCT GAA GAC TCA GTC AAC AAT ATC	384
Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile	
35 40 45	
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAC GAC TCT	432
Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser	
50 55 60	
GGA ACG CCT GTT GTC ACC TCC GGA TGC CTA GGA CTA GAA GGG TCA GAT	480
Gly Thr Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp	
65 70 75	

TTT	CAA	TGT	CGC	GAC	ACG	CCC	ATC	CCT	CAT	CAG	AGA	AGG	TCA	ATT	GAA	528
Phe	Gln	Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	
80						85					90					
TGC	TGC	ACA	GAA	AGG	AAC	GAA	TGT	AAT	AAA	GAT	CTC	CAC	CCC	ACG	CTG	576
Cys	Cys	Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	
95					100					105					110	
CCT	CCC	CTG	AAG	GAC	AGA	GAT	TTT	GTT	GAT	GGA	CCC	ATA	CAC	CAC	AAA	624
Pro	Pro	Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	
				115					120					125		
GCC	TTA	CTC	ATA	TCT	GTG	ACT	GTC	TGT	AGT	TTA	CTC	TTG	GTC	CTC	ATT	672
Ala	Leu	Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	
			130					135					140			
ATT	TTA	TTC	TGT	TAC	TTC	AGG	TAT	AAA	AGA	CAA	GAA	GCC	AGA	CCT	CGG	720
Ile	Leu	Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	
		145					150					155				
TAC	AGC	ATT	GGG	CTG	GAG	CAG	GAT	GAA	ACG	TAC	ATT	CCT	CCT	GGA	GAA	768
Tyr	Ser	Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	
	160					165					170					
TCC	CTG	AGA	GAC	TTG	ATT	GAG	CAA	TCG	CAG	AGC	TCG	GGA	AGT	GGC	TCA	816
Ser	Leu	Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	
175					180					185					190	
GGA	CTC	CCT	CTG	CTG	GTC	CAA	AGG	ACA	ATA	GCT	AAG	CAA	ATT	CAG	ATG	864
Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	
				195					200					205		
GTG	AAG	CAA	ATT	GGA	AAA	GGT	CGC	TAT	GGC	GAA	GTG	TGG	ATG	GGA	AAG	912
Val	Lys	Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	
			210					215					220			
TGG	CGT	GGA	GAA	AAG	GTA	GCT	GTG	AAA	GTG	TTC	TTC	ACC	ACG	GAG	GAA	960
Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	
		225					230					235				
GCC	AGC	TGG	TTC	CGA	GAG	ACT	GAG	ATA	TAT	CAG	ACG	GTC	CTG	ATG	AGG	1008
Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	
	240					245					250					
CAC	GAG	AAC	ATT	CTG	GGG	TTC	ATT	GCA	GCA	GAT	ATC	AAA	GGG	ACT	GGG	1056
His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	
255					260					265					270	
TCT	TGG	ACT	CAG	TTA	TAC	CTC	ATC	ACA	GAC	TAT	CAT	GAA	AAC	GGG	TCT	1104
Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	
				275					280					285		
CTT	TAT	GAC	TAT	CTG	AAA	TCC	ACC	ACC	TTA	GAT	GCC	AAG	TCC	ATG	CTG	1152
Leu	Tyr	Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	
			290					295					300			
AAG	CTA	GCC	TAC	TCG	TCT	GTC	AGC	GGC	CTG	TGC	CAT	CTA	CAC	ACG	GAA	1200
Lys	Leu	Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	
		305					310					315				

ATC TTC AGC ACT CAA GGC AAG CCA GCC ATT GCC CAT CGG GAC TTG AAA Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys 320 325 330	1248
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp 335 340 345 350	1296
CTG GGC CTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATT Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile 355 360 365	1344
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val 370 375 380	1392
CTG GAC GAG AGC TTG AAT AGA ACT CAT TTC CAG TCC TAC ATC ATG GCT Leu Asp Glu Ser Leu Asn Arg Thr His Phe Gln Ser Tyr Ile Met Ala 385 390 395	1440
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys 400 405 410	1488
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCA TAT CAC GAC CTG Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu 415 420 425 430	1536
GTG CCC AGT GAC CCC TCT TAT GAG GAC ATG AGA GAA ATT GTG TGT ATG Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met 435 440 445	1584
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAC GAG TGC Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys 450 455 460	1632
CTC AGG CAA ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAT AAT CCT Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala His Asn Pro 465 470 475	1680
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACA CTT GCC AAA ATG Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met 480 485 490	1728
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGG TACTTGTGGA CAGAGCAAGG Ser Glu Ser Gln Asp Ile Lys Leu 495 500	1782
AATTACACAG AAGCATCCTT AGCCCAAGCC TTGAACGTTG ATCTACTGCC CAGTGAGTTC	1842
AGACTTTCCT CTAAGAGAGC AAGCTGGACA GACACAGAGG AACCCAGAAA CACGGCTTCA	1902
CCATGGCTTT CTGAGGAGGG GAAACCATTT GGGTAACTTG TTCAAGATAT GATGCATGTT	1962
GCTTTCTAAG AAAGCCCTGT ATTTTGGGAT TACCATTTTT TTAAAGAAG AAAGATACTT	2022
TAATTTTAC CAAAATAAAA CAAATATTAT AGAAAAAAG CGGCCGCAGA ATTC	2076

(2) INFORMATION FOR SEQ ID NO:4:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Leu	Leu	Arg	Ser	Ser	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys	Lys	Glu	1	5	10	15
Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Ala	Arg	Pro	Lys	Val	Leu	Arg	Cys	20	25	30	
Lys	Cys	His	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser	35	40	45	
Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	Gly	Thr	50	55	60	
Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln	65	70	75	80
Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	Cys	Cys	85	90	95	
Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	Pro	Pro	100	105	110	
Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	Ala	Leu	115	120	125	
Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	Ile	Leu	130	135	140	
Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	Tyr	Ser	145	150	155	160
Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	Ser	Leu	165	170	175	
Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	180	185	190	
Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Lys	195	200	205	
Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	210	215	220	
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	225	230	235	240
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	245	250	255	
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	260	265	270	
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	275	280	285	

Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
 290 295 300
 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
 305 310 315 320
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
 325 330 335
 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
 340 345 350
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
 355 360 365
 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
 370 375 380
 Glu Ser Leu Asn Arg Thr His Phe Gln Ser Tyr Ile Met Ala Asp Met
 385 390 395 400
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser
 405 410 415
 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro
 420 425 430
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys
 435 440 445
 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg
 450 455 460
 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala His Asn Pro Ala Ser
 465 470 475 480
 Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu
 485 490 495
 Ser Gln Asp Ile Lys Leu
 500

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: CFK1-10a

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 474..2000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCTGCG GCCGCGAGGC TGCATTAAGT GGGATATGCC ACCCGTGATT CTGACAGCCG	60
TGACTGCGTG GAGCCTGCTC CGGAACTCTC CACAGAGGAG CAAAGGAGCT GCCCTCTGTG	120
TCTCCCCGCC CTTCAGCGAG AGTCTGGAAA GAGAACCGAG GTGCTACTGC AGTGGATGAG	180
TAGAGAAGAG TCTGCATCCA GTGCTGGTGA GCTTGTCTGG CTATAGGGAG CCTGCTGGGG	240
GAAACTTACA GCTTCAGAAG ACTCCTGGAG AGCCTCTCCC TCCACACTCT CCCTTTGAGC	300
AGTCAGTGCC TCTCTGCTGG AGAACCTGTG CTGGGTGTGC CCCAGAGCTG GCTTTGACTG	360
TAGCCTGTCA GGCTCTCCCT GGACCTCACG GAACAGCATT GCCAGCCACA CGGCTTCCAA	420
CAAATCACCT CTTTTCATGC TGTTTGGCAC AGATCGAATC TACAGGTTAT ACA ATG	476
	Met 1
GTC GAT GGA GCA ATG ATC CTT TCT GTG CTA ATG ATG ATG GCT CTC CCT	524
Val Asp Gly Ala Met Ile Leu Ser Val Leu Met Met Met Ala Leu Pro	
	5 10 15
TCC CCG AGT ATG GAA GAT GAG GAG CCC AAG GTC AAC CCG AAG CTT TAC	572
Ser Pro Ser Met Glu Asp Glu Glu Pro Lys Val Asn Pro Lys Leu Tyr	
	20 25 30
ATG TGT GTG TGT GAG GGC CTC TCC TGC GGG AAC GAG GAC CAC TGT GAG	620
Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu	
	35 40 45
GGC CAG CAG TGT TTT TCC TCC CTG AGC GTC AAT GAT GGC TTC CGC GTC	668
Gly Gln Gln Cys Phe Ser Ser Leu Ser Val Asn Asp Gly Phe Arg Val	
	50 55 60 65
TAC CAG AAG GGC TGC TTT CAG GTC TAT GAG CAG GGG AAG ATG ACG TGT	716
Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys	
	70 75 80
AAG ACC CCG CCG TCG CCT GGC CAG GCT GTG GAG TGC TGC CAA GGG GAC	764
Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp	
	85 90 95
TGG TGC AAC AGG AAC GTC ACG GCC CGG CTG CCC ACT AAA GGG AAA TCC	812
Trp Cys Asn Arg Asn Val Thr Ala Arg Leu Pro Thr Lys Gly Lys Ser	
	100 105 110
TTC CCT GGA TCG CAG AAC TTC CAC CTG GAA GTT GGC CTT ATC ATC CTC	860
Phe Pro Gly Ser Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu	
	115 120 125
TCC GTG GTG TTT GCG GTA TGC CTT TTC GCT TGC ATC CTT GGC GTT GCT	908
Ser Val Val Phe Ala Val Cys Leu Phe Ala Cys Ile Leu Gly Val Ala	
	130 135 140 145
CTC AGG AAG TTT AAA AGG CGC AAT CAA GAG CGC CTG AAC CCC AGA GAC	956
Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp	
	150 155 160

GTG GAG TAC GGT ACT ATC GAA GGG CTC ATC ACC ACC AAC GTC GGA GAT	1004
Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp	
165 170 175	
AGC ACT CTA GCG GAA TTA CTA GAT CAC TCA TGT ACA TCA GGA AGT GGC	1052
Ser Thr Leu Ala Glu Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly	
180 185 190	
TCC GGT CTT CCT TTT CTG GTA CAG AGA ACT GTG GCT CGA CAG ATA ACC	1100
Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr	
195 200 205	
CTG TTG GAG TGT GTC GGG AAG GGC CGG TAT GGA GAA GTG TGG AGG GGC	1148
Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly	
210 215 220 225	
AGC TGG CAA GGC GAA AAT GTT GCT GTG AAG ATC TTC TCC TCC CGT GAT	1196
Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp	
230 235 240	
GAG AAG TCG TGG TTC AGG GAG ACA GAA TTG TAC AAC ACG GTG ATG CTG	1244
Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu	
245 250 255	
AGG CAT GAG AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACC TCT AGA	1292
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg	
260 265 270	
CAC TCC AGT ACC CAG CTG TGG CTC ATT ACA CAT TAC CAC GAA ATG GGA	1340
His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly	
275 280 285	
TCG TTG TAT GAC TAC CTT CAG CTC ACC ACT CTG GAC ACC GTT AGC TGC	1388
Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys	
290 295 300 305	
CTT CGG ATC GTG TTG TCC ATA GCC AGC GGC CTT GCA CAC TTG CAC ATA	1436
Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile	
310 315 320	
GAG ATA TTT GGG ACC CAG GGG AAG TCT GCC ATC GCC CAC CGA GAT CTA	1484
Glu Ile Phe Gly Thr Gln Gly Lys Ser Ala Ile Ala His Arg Asp Leu	
325 330 335	
AAG AGC AAA AAC ATC CTC GTG AAG AAG AAC GGA CAG TGC TGC ATA GCA	1532
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala	
340 345 350	
GAT TTG GGC CTG GCA GTC ATG CAT TCC CAG AGC ACG AAT CAG CTT GAT	1580
Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp	
355 360 365	
GTG GGA AAC AAC CCC CGT GTG GGG ACC AAG CGC TAC ATG GCC CCT GAA	1628
Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu	
370 375 380 385	
GTG CTT GAT GAA ACC ATC CAA GTG GAT TGC TTT GAT TCT TAT AAG AGG	1676
Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg	
390 395 400	

GTC GAT ATT TGG GCC TTT GGC CTC GTT CTG TGG GAA GTG GCC AGG AGG Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg 405 410 415	1724
ATG GTG AGC AAT GGT ATA GTG GAA GAT TAC AAG CCA CCA TTC TAT GAT Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp 420 425 430	1772
GTT GTT CCC AAT GAC CCA AGT TTT GAA GAT ATG AGG AAA GTT GTC TGT Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys 435 440 445	1820
GTG GAT CAA CAG AGG CCA AAC ATA CCT AAC AGA TGG TTC TCA GAC CCG Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro 450 455 460 465	1868
ACA TTA ACT TCT CTG GCG AAG CTG ATG AAA GAA TGC TGG TAC CAG AAC Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn 470 475 480	1916
CCA TCC GCC AGA CTC ACA GCT CTA CGT ATC AAA AAG ACT TTG ACC AAA Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys 485 490 495	1964
ATT GAT AAC TCC CTA GAC AAA TTA AAA ACT GAC TGT TGACATTGTC Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys 500 505	2010
ACCGGTGTCA AGAAGGAGAG TCAATGCTGT CATTGTCCAG CTGGGACCTA ATGCTGGCCT	2070
GACTGGTTGT CAGAACAGAA TCCATCTGTC CCCCTCTCCC CCCAACTCCC GAAGTGGCTG	2130
CTTTGACAAA AGCAGATGTC TCTTCCCAGC CATGTTCCGG GGGAGACACC AAAACCACCC	2190
TAACCTCGCT CAGAACTGT GACTCGAGCA CTTGATGAAC TGTTACACACC GCAAAGACTA	2250
ACGGTGGGCA GGTATGTTTG CAAGGGGGAG GGAAGTGGAG GAGCACAGAG AGATCCTGCA	2310
GGAGATCTGG GCATTAGGAC AGTGGCTCTT TGCATATCTT CCACGGGTCT CCTAGACTCG	2370
CCCCACGGGA AACTCAAGGA GGCGGTGAAT TCGTAATCAG CAATATTGGC TCGCGCTACT	2430
CTTCTCTGTT GCACTAGGAA TTCTCTGCAT TCCTTACTTG CACTGTCGTC CTTAATCTTA	2490
AAGACCCGAC TTGCCAAAAC ATTGGCTGCC TACTTCACTG GCCTGTCTCT GGACAATAGG	2550
AATTCAATCT GGCAGAACAA AAATGTAATG TTGGACTTTG CTGCATTTTA CACACGTGCC	2610
GATGTTTACA ACGATGCAAA CATTAGGAAT TGTTTAGACA CAACTTTGCA AATTATTTAT	2670
TACTGGTGCA CTTAGCAGTT TTTGTTTTTT TTTGTTTTTT TGTTTTTTTT TTGTTTTGTT	2730
TTGTTTTTAT ATATAAACT GCCTCGTGCG TATGTTAAAG CTTATTTTTA TGTGGTCTTA	2790
TGATTTTATT ACCGAAATGT TTTAACACC CGATTCTGAA ATGGATGTTT TCTTTTATTA	2850
TCAGTTAAAT TCACATTTTA AATGCTTCAC TTTTTTTTTA TGTGTGTAGA CTGTAACTTT	2910
CTTTTCAGTT AGTATACAGA ACGTATTTAG CCATTACCCA TGCAACACCA CCCAATATAT	2970
TACTGATTTA GAAGCAAAGA TTTCACTAGA ATTTTAGTCC CAAACGCTGT GGGGGGGAAA	3030

TGCATCTTCT TCGGAACATAT CCATTACATG CATTTAAACT CTGCCAGAAA AAAAAATAAC	3090
TATTTTGTTT TAATCTACTT TTTGTATTTA GTAGTTATTT GTATAAATTA AATAAACTGT	3150
TTTCAAGTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAT	3210
AAAAAAAAAA AAAGCGGCCG CAGAATTC	3238

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Val	Asp	Gly	Ala	Met	Ile	Leu	Ser	Val	Leu	Met	Met	Met	Ala	Leu	1	5	10	15
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Glu	Pro	Lys	Val	Asn	Pro	Lys	Leu	20	25	30	
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys	35	40	45	
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Ser	Leu	Ser	Val	Asn	Asp	Gly	Phe	Arg	50	55	60	
Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr	65	70	75	80
Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly	85	90	95	
Asp	Trp	Cys	Asn	Arg	Asn	Val	Thr	Ala	Arg	Leu	Pro	Thr	Lys	Gly	Lys	100	105	110	
Ser	Phe	Pro	Gly	Ser	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile	115	120	125	
Leu	Ser	Val	Val	Phe	Ala	Val	Cys	Leu	Phe	Ala	Cys	Ile	Leu	Gly	Val	130	135	140	
Ala	Leu	Arg	Lys	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg	145	150	155	160
Asp	Val	Glu	Tyr	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly	165	170	175	
Asp	Ser	Thr	Leu	Ala	Glu	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser	180	185	190	
Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile	195	200	205	
Thr	Leu	Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	210	215	220	

Gly	Ser	Trp	Gln	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	225	230	235	240
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met	245	250	255	
Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	260	265	270	
Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met	275	280	285	
Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser	290	295	300	
Cys	Leu	Arg	Ile	Val	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala	His	Leu	His	305	310	315	320
Ile	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Ser	Ala	Ile	Ala	His	Arg	Asp	325	330	335	
Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Gln	Cys	Cys	Ile	340	345	350	
Ala	Asp	Leu	Gly	Leu	Ala	Val	Met	His	Ser	Gln	Ser	Thr	Asn	Gln	Leu	355	360	365	
Asp	Val	Gly	Asn	Asn	Pro	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	370	375	380	
Glu	Val	Leu	Asp	Glu	Thr	Ile	Gln	Val	Asp	Cys	Phe	Asp	Ser	Tyr	Lys	385	390	395	400
Arg	Val	Asp	Ile	Trp	Ala	Phe	Gly	Leu	Val	Leu	Trp	Glu	Val	Ala	Arg	405	410	415	
Arg	Met	Val	Ser	Asn	Gly	Ile	Val	Glu	Asp	Tyr	Lys	Pro	Pro	Phe	Tyr	420	425	430	
Asp	Val	Val	Pro	Asn	Asp	Pro	Ser	Phe	Glu	Asp	Met	Arg	Lys	Val	Val	435	440	445	
Cys	Val	Asp	Gln	Gln	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Phe	Ser	Asp	450	455	460	
Pro	Thr	Leu	Thr	Ser	Leu	Ala	Lys	Leu	Met	Lys	Glu	Cys	Trp	Tyr	Gln	465	470	475	480
Asn	Pro	Ser	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Thr	485	490	495	
Lys	Ile	Asp	Asn	Ser	Leu	Asp	Lys	Leu	Lys	Thr	Asp	Cys				500	505		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
(B) CLONE: W-101

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 80..1594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATCTGCGG CCGCGAGGGA GAGAGGCGCC GGGGGCGCGC GCGCGCGCTG GGCGCTGCTG	60
GGCTGCGGCG GCGGTTACT ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC	112
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe	
1 5 10	
CCC CTT GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG	160
Pro Leu Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg	
15 20 25	
GGG ATC CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC	208
Gly Ile Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn	
30 35 40	
TAC ACC TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG	256
Tyr Thr Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu	
45 50 55	
GAT GGC GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG	304
Asp Gly Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu	
60 65 70 75	
GTT CCT GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC	352
Val Pro Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg	
80 85 90	
AAC ACA CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG	400
Asn Thr His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg	
95 100 105	
GTC CCC AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC	448
Val Pro Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly	
110 115 120	
CCT GTG GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC	496
Pro Val Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe	
125 130 135	
CTT ATC ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC	544
Leu Ile Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val	
140 145 150 155	
TAC CAT AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG	592
Tyr His Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met	
160 165 170	

TGT	CTC	TCC	AAA	GAC	AAG	ACG	CTC	CAG	GAT	CTC	GTC	TAC	GAC	CTC	TCC	640
Cys	Leu	Ser	Lys	Asp	Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	
			175					180					185			
ACG	TCA	GGG	TCT	GGC	TCA	GGG	TTA	CCC	CTT	TTT	GTC	CAG	CGC	ACA	GTG	688
Thr	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	
		190					195					200				
GCC	CGA	ACC	ATT	GTT	TTA	CAA	GAG	ATT	ATC	GGC	AAG	GGC	CGG	TTC	GGG	736
Ala	Arg	Thr	Ile	Val	Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	
	205					210					215					
GAA	GTA	TGG	CGT	GGT	CGC	TGG	AGG	GGT	GGT	GAC	GTG	GCT	GTG	AAA	ATC	784
Glu	Val	Trp	Arg	Gly	Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	
220					225					230					235	
TTC	TCT	TCT	CGT	GAA	GAA	CGG	TCT	TGG	TTC	CGT	GAA	GCA	GAG	ATC	TAC	832
Phe	Ser	Ser	Arg	Glu	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	
			240					245						250		
CAG	ACC	GTC	ATG	CTG	CGC	CAT	GAA	AAC	ATC	CTT	GGC	TTT	ATT	GCT	GCT	880
Gln	Thr	Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	
			255					260					265			
GAC	AAT	AAA	GAT	AAT	GGC	ACC	TGG	ACC	CAG	CTG	TGG	CTT	GTC	TCT	GAC	928
Asp	Asn	Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	
		270					275					280				
TAT	CAC	GAG	CAT	GGC	TCA	CTG	TTT	GAT	TAT	CTG	AAC	CGC	TAC	ACC	GTG	976
Tyr	His	Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	
	285					290					295					
ACC	ATT	GAG	GGC	ATG	ATT	AAG	CTA	GCC	TTG	TCT	GCA	GCC	AGT	GGT	TTG	1024
Thr	Ile	Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	
300					305					310					315	
GCA	CAC	CTG	CAT	ATG	GAG	ATT	GTG	GGC	ACT	CAA	GGG	AAG	CCG	GGA	ATT	1072
Ala	His	Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	
			320					325						330		
GCT	CAT	CGA	GAC	TTG	AAG	TCA	AAG	AAC	ATC	CTG	GTG	AAA	AAA	AAT	GGC	1120
Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	
			335				340						345			
ATG	TGT	GCC	ATT	GCA	GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCG	GTC	1168
Met	Cys	Ala	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	
		350				355						360				
ACT	GAC	ACC	ATA	GAC	ATT	GCT	CCA	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	1216
Thr	Asp	Thr	Ile	Asp	Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	
	365					370					375					
TAC	ATG	GCT	CCT	GAA	GTC	CTT	GAC	GAG	ACA	ATC	AAC	ATG	AAG	CAC	TTT	1264
Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	
380					385					390					395	
GAC	TCC	TTC	AAA	TGT	GCC	GAC	ATC	TAT	GCC	CTC	GGG	CTT	GTC	TAC	TGG	1312
Asp	Ser	Phe	Lys	Cys	Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	
				400					405					410		

GAG ATT GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA	1360
Glu Ile Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln	
415 420 425	
CTG CCG TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG	1408
Leu Pro Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met	
430 435 440	
CGA AAG GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG	1456
Arg Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp	
445 450 455	
TGG CAG AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG	1504
Trp Gln Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu	
460 465 470 475	
TGC TGG TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG	1552
Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys	
480 485 490	
AAG ACT CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT	1594
Lys Thr Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile	
495 500 505	
TAAGCTGTTA AGATGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGG	1647

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu	
1 5 10 15	
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu	
20 25 30	
Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr	
35 40 45	
Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His	
50 55 60	
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys	
65 70 75 80	
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys	
85 90 95	
Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His	
100 105 110	
Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val	
115 120 125	

Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
 130 135 140
 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
 145 150 155 160
 Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
 165 170 175
 Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
 180 185 190
 Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
 195 200 205
 Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
 210 215 220
 Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
 225 230 235 240
 Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
 245 250 255
 Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
 260 265 270
 Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
 275 280 285
 Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
 290 295 300
 Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
 305 310 315 320
 Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
 325 330 335
 Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
 340 345 350
 Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
 355 360 365
 Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
 370 375 380
 Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
 385 390 395 400
 Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
 405 410 415
 Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp
 420 425 430
 Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
 435 440 445
 Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu
 450 455 460

Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
 465 470 475 480
 Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
 485 490 495
 Leu Ser Val Gln Glu Asp Val Lys Ile
 500 505

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: W-120

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 83..1591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGCGG CCGCGGGCGA GGCTTCCTGA GGAGAAGCTG CGGCCGGGGC CGGGCCGGGC	60
CACAAACAGT GCGGCGGGGA CC ATG GAG GCG GCG GCC GCT GCT CCA CGT CGT	112
Met Glu Ala Ala Ala Ala Ala Pro Arg Arg	10
1 5	
CCG CAG CTC CTC ATC GTG TTG GTG GCG GCG GCG ACG CTG CTC CCG GGG	160
Pro Gln Leu Leu Ile Val Leu Val Ala Ala Ala Thr Leu Leu Pro Gly	25
15 20	
GCG AAG GCA TTA CAG TGT TTC TGC CAC CTC TGT ACA AAG GAT AAT TTT	208
Ala Lys Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe	40
30 35	
ACC TGT GAG ACA GAT GGT CTT TGC TTT GTC TCA GTC ACT GAG ACC ACA	256
Thr Cys Glu Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr	55
45 50	
GAC AAA GTT ATA CAC AAT AGT ATG TGT ATA GCT GAA ATT GAC CTA ATT	304
Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile	70
60 65	
CCT CGA GAC AGG CCA TTT GTA TGT GCA CCA TCT TCA AAA ACA GGG GCA	352
Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ala	90
75 80	
GTT ACT ACA ACA TAT TGC TGC AAT CAG GAC CAC TGC AAT AAA ATA GAA	400
Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu	105
95 100	
CTC CCA ACT ACA GGA CCT TTT TCA GAA AAG CAG TCA GCT GGC CTT GGT	448
Leu Pro Thr Thr Gly Pro Phe Ser Glu Lys Gln Ser Ala Gly Leu Gly	120
110 115	

CCT	GTG	GAG	CTG	GCA	GCT	GTC	ATT	GCT	GGT	CCA	GTC	TGC	TTC	GTC	TGC	496
Pro	Val	Glu	Leu	Ala	Ala	Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	
		125					130					135				
ATT	GCA	CTT	ATG	CTG	ATG	GTC	TAT	ATC	TGC	CAT	AAC	CGC	ACT	GTC	ATT	544
Ile	Ala	Leu	Met	Leu	Met	Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	
	140					145					150					
CAC	CAC	CGT	GTG	CCA	AAT	GAA	GAG	GAT	CCA	TCA	CTA	GAT	CGC	CCT	TTC	592
His	His	Arg	Val	Pro	Asn	Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	
155					160					165					170	
ATT	TCA	GAG	GGC	ACC	ACC	TTA	AAA	GAT	TTA	ATT	TAT	GAT	ATG	ACA	ACA	640
Ile	Ser	Glu	Gly	Thr	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	
				175					180					185		
TCA	GGG	TCT	GGA	TCA	GGT	TTA	CCA	CTG	CTT	GTT	CAA	AGA	ACA	ATT	GCC	688
Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	
			190					195					200			
AGG	ACC	ATT	GTG	TTA	CAA	GAA	AGC	ATT	GGC	AAA	GGT	CGG	TTT	GGA	GAA	736
Arg	Thr	Ile	Val	Leu	Gln	Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	
		205					210					215				
GTT	TGG	CGA	GGC	AAA	TGG	CGG	GGA	GAA	GAA	GTT	GCT	GTG	AAG	ATA	TTC	784
Val	Trp	Arg	Gly	Lys	Trp	Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	
	220					225					230					
TCT	TCT	AGA	GAA	GAG	CGT	TCA	TGG	TTC	CGA	GAG	GCA	GAG	ATT	TAT	CAG	832
Ser	Ser	Arg	Glu	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	
235					240					245					250	
ACT	GTA	ATG	TTA	CGC	CAT	GAA	AAT	ATC	CTG	GGA	TTT	ATA	GCA	GCA	GAC	880
Thr	Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	
				255					260				265			
AAC	AAA	GAC	AAT	GGG	ACA	TGG	ACG	CAG	CTG	TGG	TTG	GTG	TCA	GAT	TAT	928
Asn	Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	
			270					275					280			
CAT	GAG	CAT	GGA	TCC	CTT	TTC	GAT	TAC	TTG	AAT	AGA	TAC	ACT	GTT	ACT	976
His	Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	
		285					290					295				
GTG	GAA	GGA	ATG	ATC	AAG	CTT	GCT	CTG	TCC	ACA	GCA	AGT	GGT	CTT	GCC	1024
Val	Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	
	300					305					310					
CAT	CTT	CAC	ATG	GAG	ATT	GTT	GGT	ACC	CAA	GGA	AAA	CCA	GCT	ATT	GCC	1072
His	Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	
315					320					325					330	
CAT	AGA	GAT	TTG	AAA	TCA	AAG	AAT	ATC	TTG	GTG	AAG	AAA	AAT	GGA	ACC	1120
His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	
				335					340					345		
TGT	TGT	ATT	GCA	GAC	TTG	GGA	CTT	GCT	GTG	AGA	CAT	GAT	TCT	GCC	ACA	1168
Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	
			350					355					360			

GAT ACA ATT GAT ATT GCT CCA AAC CAC AGA GTA GGC ACT AAA AGG TAC	1216
Asp Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr	
365 370 375	
ATG GCC CCT GAA GTT CTA GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA	1264
Met Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu	
380 385 390	
TCC TTC AAA CGC GCT GAC ATC TAT GCA ATG GGC TTA GTG TTC TGG GAA	1312
Ser Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu	
395 400 405 410	
ATT GCT CGA CGC TGT TCT ATT GGT GGA ATC CAT GAA GAC TAT CAG TTG	1360
Ile Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu	
415 420 425	
CCT TAT TAT GAT CTT GTA CCT TCT GAT CCA TCG GTT GAA GAA ATG AGA	1408
Pro Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg	
430 435 440	
AAA GTA GTT TGC GAA CAG AAG TTA AGG CCA AAT ATT CCA AAC AGA TGG	1456
Lys Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp	
445 450 455	
CAG AGC TGT GAG GCC TTG AGA GTG ATG GCT AAA ATT ATG AGA GAA TGC	1504
Gln Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys	
460 465 470	
TGG TAT GCC AAT GGA GCA GCA AGG CTG ACA GCT TTG CGA ATT AAA AAA	1552
Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys	
475 480 485 490	
ACA TTG TCA CAA CTC AGC CAA CAG GAA GGC ATC AAA ATG TAACTGAAAC	1601
Thr Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met	
495 500	
ACCGTGGGAA CTCTGCTCTC TTCATATCTG CTCCTGGGTG TTAGGAGGC TGGTTGTTCT	1661
ACCTCACTGA GAGAACAGAG GGCTCTGCTT CCTCTTGCAG CAGTGAATA TGGTCAACTG	1721
AAAGCTTCCC AGGGTTTCTC TGGGCCAGA GGCAGCCGTG GGGTCCTTCT GTGCACTATG	1781
GATAACTTCT TCC	1794

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Ala Ala Ala Ala Ala Pro Arg Arg Pro Gln Leu Leu Ile Val
1 5 10 15
Leu Val Ala Ala Ala Thr Leu Leu Pro Gly Ala Lys Ala Leu Gln Cys
20 25 30

Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys Glu Thr Asp Gly
35 40 45
Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys Val Ile His Asn
50 55 60
Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg Asp Arg Pro Phe
65 70 75 80
Val Cys Ala Pro Ser Ser Lys Thr Gly Ala Val Thr Thr Thr Tyr Cys
85 90 95
Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro Thr Thr Gly Pro
100 105 110
Phe Ser Glu Lys Gln Ser Ala Gly Leu Gly Pro Val Glu Leu Ala Ala
115 120 125
Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ala Leu Met Leu Met
130 135 140
Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn
145 150 155 160
Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr
165 170 175
Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly
180 185 190
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln
195 200 205
Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp
210 215 220
Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg
225 230 235 240
Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His
245 250 255
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr
260 265 270
Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu
275 280 285
Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys
290 295 300
Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile
305 310 315 320
Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser
325 330 335
Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu
340 345 350
Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala
355 360 365

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
370 375 380

Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
385 390 395 400

Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
405 410 415

Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
420 425 430

Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
435 440 445

Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
450 455 460

Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
465 470 475 480

Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
485 490 495

Gln Gln Glu Gly Ile Lys Met
500

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: KDA-B5

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 25..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATCCGAAT ACGTGGCGGT TAAA ATA TTC TCC TCC AGG GAT GAG AGA TCT	51
Ile Phe Ser Ser Arg Asp Glu Arg Ser	
1 5	
TGG TTC CGT GAG GCG GAA ATT TAT CAG ACG GTG ATG CTG AGA CAC GAG	99
Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His Glu	
10 15 20 25	
AAC ATC CTC GGT TTC ATC GCA GCT GAC AAC AAA GAT AAT GGA ACT TGG	147
Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr Trp	
30 35 40	
ACA CAA CTC TGG CTT GTG TCA GAG TAT CAC GAG CAG GGC TCC TTG TAT	195
Thr Gln Leu Trp Leu Val Ser Glu Tyr His Glu Gln Gly Ser Leu Tyr	
45 50 55	

GAC TAT TTG AAC AGA AAC ATA GTG ACT GTG GCT GGA ATG GTC AAG CTG	243
Asp Tyr Leu Asn Arg Asn Ile Val Thr Val Ala Gly Met Val Lys Leu	
60 65 70	
GCG CTT TCC ATA GCG AGT GGT CTG GCT CAC CTG CAC ATG GAG ATC GTG	291
Ala Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Met Glu Ile Val	
75 80 85	
GGT ACT CAA GGT AAG CTT GCT ATT GCT CACGGTGATA TCAAAAGTCT	338
Gly Thr Gln Gly Lys Leu Ala Ile Ala	
90 95	
AGA	341

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Phe Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile
1 5 10 15
Tyr Gln Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala
20 25 30
Ala Asp Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser
35 40 45
Glu Tyr His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile
50 55 60
Val Thr Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser Gly
65 70 75 80
Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Leu Ala
85 90 95
Ile Ala

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PRIMER A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGGATCCGA RTAYGTNGCN GTNAAR

26

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PRIMER B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACTGTAGAR CTYTTDATRT CYCTRTG

27

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PRIMER C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GACTCTAGAR CTYTTDATRT CNCGRTG

27

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PRIMER D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GACTCTAGNG AYTTDATRTC YCTRTG

26

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
(B) CLONE: PRIMER E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTCTAGAN GAYTTDATRT CNCGRTG

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
(B) CLONE: PEPTIDE SEQUENCE OF KDA-B5 USED TO DESIGN
PRIMER A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Glu Tyr Val Ala Val Lys
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
(B) CLONE: PEPTIDE SEQUENCE OF KDA-B5 USED TO DESIGN
PRIMERS B THRU E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Arg Asp Ile Lys Ser
1 5